```
***********************************
# Program: needle
# Rundate: Mon Sep 11 20:02:59 2006
# Align format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060911-20025882318727.output
#
# Aligned sequences: 2
# 1: SEQ 179
# 2: G_kaustophilus_holB
# Matrix: EBLOSUM62
# Gap penalty: 10.0
# Extend_penalty: 0.5
# Length: 987
           754/987 (76.4%)
# Identity:
           754/987 (76.4%)
# Similarity:
           230/987 (23.3%)
# Gaps:
# Score: 4576.0
1 atgcgatgggaacagctagcgaaacgccagccggtggtggcgaaaatgct
                                                       50
SEQ_179
               {\tt 1} \ {\tt atgcgatgggaacagctagcgaaacgccagccggtggtggcgaaaatgct}
                                                      50
G_kaustophilu
                                                      100
             51 gcaaagcggcttggaaaaagggcggatttctcatgcgtacttgtttgagg
SEQ 179
               51 gcaaageggcttggaaaaagggeggattteteatgegtacttgtttgagg
                                                      1.00
G kaustophilu
            101 qqcaqcqqqqacqqqcaaaaaagcggccagtttgttgttggcgaaacgt
                                                      150
SEQ_179
               101 ggcagcggggacgggcaaaaaagcggccagtttgttgttggcgaaacgt
                                                      150
G kaustophilu
            151 ttqttttgtctgtccccaatcggagtttccccgtgtctagagtgccgcaa
                                                      200
SEQ_179
               151 ttgttttgtctgtccccaatcggagtttccccgtgtctagagtgccgcaa
                                                      200
G kaustophilu
            201 ctgccggcgcatcgactccggcaaccaccctgacgtccgggtgatcggcc
                                                      250
SEQ 179
               201 ctgccggcgcatcgactccggcaaccaccctgacgtccgggtgatcagcc
                                                      250
G kaustophilu
                                                      300
            251 caqatqqaqqatcaatcaaaaaggaacaaatcgaatggctgcagcaagag
SEQ 179
               251 cagacggaggatcaatcaaaaaggaacaaatcgaatggctgcagcaagag
                                                      300
G_kaustophilu
SEQ_179
            301 ttctcqaaaacaqcqqtcgagtcggataaaaaaatgtacatcgttgagca
                                                      350
               301 ttctcgaaaacagcggtcgagtcggataaaaaaatgtacatcgttgagca
                                                      350
G kaustophilu
                                                      400
            351 cgccgatcaaatgacgacaagcgctgccaacagccttctgaaatttttgg
SEQ 179
               351 cgccgatcaaatgacgacaagcgctgccaacagccttctgaaatttttgg
                                                      400
G_kaustophilu
                                                      450
            SEQ 179
               450
G kaustophilu
            451 cgcctgctagggacgatcgtttcccgctgtcaagtgctttcgttccggcc
                                                     500
SEQ_179
               500
G kaustophilu
            451 egectgetagggaegategttteeegetgteaagtgetttegtteeggee
```

SEQ_179	501 gttgeegeeggeagagetegeeeagggaettgtegaggag	cacgtgccgt	550
G_kaustophilu	501 gttgccgccggcagagctcgctcagggacttgtcgaggag	cacgtgccgt	550
SEQ_179	551 tgccgttggcgctgttggctgcccatttgacaaacagctt	cgaggaagca	600
G_kaustophilu	551 tgccgttggcgctgttggctgcccatttgacaaacagctt	cgaggaagca	600
SEQ_179	601 ctggcgcttgccaaagatagttggtttgccgaggcgcgaa	cattagtgct	650
G_kaustophilu	601 ctggcgcttgccaaagatagttggtttgccgaggcgcgaa		650
SEQ_179	651 acaatggtatgagatgctgggcaagccggagctgcagctt	ttgtttttca 	700
G_kaustophilu	651 acaatggtatgagatgctgggcaagccggagctgcagctt		700
SEQ_179	701 tccacgaccgcttgtttccgcattttttggaaagccatca	gcttgacctt	750
G_kaustophilu		tccacgaccgcttgtttccgcatttttttggaaagccatcagcttgacctt	
SEQ_179	751 ggacttg 		757
G_kaustophilu	751 ggacttgatttgcttttatatttataccgcgatttgttgc	atattcaagc	800
SEQ_179	758		757
G_kaustophilu	801 cgggcagatggacggcgtgttataccgcgatcagctggac	cgcctgcaac	850
SEQ_179	758		757
G_kaustophilu	851 gatgggcgcttgcttgcccgcagcggcggattttggctgg	catggaagcg	900
SEQ_179	758		757
G_kaustophilu	901 attttacaagcgaaaacgcgtttaaatacaacgaatatga	gcacggcgtt	950
SEQ_179	758	757	
G kaustophilu	951 gcttgttgagcagctcgttcttcaattaaagcggtaa	987	

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